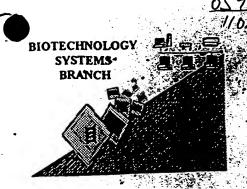0590
1/02

BIOTECHNOLOGY
SYSTEMS·
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/915706___

Source: ___OIPE___

Date Processed by STIC: ___10/17/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/915706

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY

1 _____ Wrapped Nucleics Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your fil was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequence:

8 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped seque
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represen

10 _____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknow is Artificial Sequence

11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823) of Sequence Rule

12 _____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to repre any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING   DATE: 10/17/2001
PATENT APPLICATION: US/09/915,706   TIME: 15:54:53

Input Set : A:\5112.app
Output Set: N:\CRF3\10172001\I915706.raw

```
   3 <110> APPLICANT: NELSON, DAVID R.
   5 <120> TITLE OF INVENTION: A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT
   6       PROTECTS FISH AGAINST INFECTION BY VIRULENT V.
   7       ANGUILLARUM
   9 <130> FILE REFERENCE: 5112
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/915,706 ｏｒ
C--> 12 <141> CURRENT FILING DATE: 2001-07-26 ｏｋ
  14 <160> NUMBER OF SEQ ID NOS: 4
  16 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does No Comply
Corrected ... ..te Needed

ERRORED SEQUENCES

Sæ page 2∘f4

```
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 3609
  20 <212> TYPE: DNA
  21 <213> ORGANISM: V. Anguillarum
  23 <220> FEATURE:
  24 <223> OTHER INFORMATION: "n" bases may be a, t, c, g, other or unknown
  26 <400> SEQUENCE: 1
  27 gtcgacttat tgcattgatg gcgtacatgg tagtgccatc cttcgtttgc taacaagcgt 60
  28 tgtataaaag cttggtcggt ttcatcaagt tgaacacaat actcatgatt tttcccactt 120
  29 ccggaaaggg aaaagtgaaa atagcttttg agatcagcct gttctagcag cttttcaatg 180
  30 atcttttttcg tcgttacgtt ttgaaaaatc tgacgactgc gtttgtattg caacaagcta 240
  31 agtggatcca atatctctat ttgataataa aactgctgct tgtctttgct atatcctgtg 300
  32 aattgcagag tgctacatat acctgaaaaa aaacgctttc cagaatctaa ttcgtaagac 360
  33 acacaaacag ctttacctag gttttggta tcgatctcca tgtttgccgc gatggaaacg 420
  34 gaaaactgac acccgccgga tacgctttcc tctccgatta attgcgtgac aatataactt 480
  35 ttgctatctg aaagcttaat ggtgagggag cgggtttggt gctttaattc gttactgctc 540
  36 atattcaatt aattcactat taaataaaca gttctaaaag gctgtttatt ggatgaatat 600
  37 tcgaaattat cacataataa ttgatgctat tattacttgc tgtattggta tcaactttca 660
  38 tgctctatac atgtaatata tttcgagtta gaccttaatt caaggtaatt tgtctattta 720
  39 attattatct gaataatatg taatcgattg ctttgtggtt atttttatgt ttgtttcatt 780
  40 tttaatgacg gtgagcttgt gcattcatat tttttatgat gacaacatct ttgatgaagt 840
  41 atttaagata ttgttaatgc atgagggggtt tgcgtgtatt ttttatatta aatcataata 900
  42 aaatcaacaa tatatgttat tttgtgtctt tttatagtgt tcttttaaag aggtaggatg 960
  43 acctaaaggt cgcctagaaa tatggcgtaa attgccattg ctataattca cctcaaagat 1020
  44 acactattgg caaattgaca aatatgtcac ttcgtatgaa acaatattag tagatgttgt 1080
  45 ttttgctgca aaaataaaaa tttttctggt tgaaataact caaggcctct agcgttttcc 1140
  46 tttatcttaa aatacaggaa atagcgattg aagttaattg acacttaagc aasdramgaa 1200
  47 tagtcaacct aacagagcag gaacctatgc ctttgtcaaa gcatcaaatt gagcaacttt 1260
  48 ctaaacctct gagtgatgat tcgatctgtg gcgtttatct taaactggaa aaaagtgctt 1320
  49 ttcgcccatt acgtaatgaa tttaatgtcg cgcaaactgc gctgcgtaag ctaagtcaaa 1380
  50 accctagtgc tgacgagaga gatgcgttac aagaggcatg tctaaataag tggaagattc 1440
  51 tctctgacag tttgtacgaa cagtttttcaa aaacaaccag agatatcgag ctcatctcat 1500
  52 ggtttgttgc tgctcaattc cttctcgata ccacattaga aagtgctgcg aatagccttg 1560
  53 agtggttagc ggatttaagt gagaagcact gggatcacct caaccctgta ctaccagttg 1620
```

```
                  RAW SEQUENCE LISTING                DATE: 10/17/2001
                  PATENT APPLICATION:  US/09/915,706  TIME: 15:54:53

                  Input Set : A:\5112.app
                  Output Set: N:\CRF3\10172001\I915706.raw

      54 aaacgctcaa atctgatgat gataagggca aagaaagaga gcaagcagat gcgaaagtta 1680
      55 aagcattttt ccaactagtc ggcgatagcg aggaaagctc gattctctat gcgccggtgc 1740
      56 tgcaactgcc cttagtcggg gaagtgacgt tttttgactt tcaaagtgca gagagaaaag 1800
      57 gcgaaatcag ccaactgaaa tctatgctta cgaccacggt ggcgcaagag cgtttcgcaa 1860
      58 ttcaattcaa gatggaaaac gccaaacgtt gtgtcaccca attagatcgt ttgtcagcgt 1920
      59 tggtgagcac taagtgtcat tctctaggca gtcaaagtac caacttcgga tttgcgaagt 1980
      60 cactgcttac ccgtgttgaa aacgctttgg ttcatctaag tggaattaag ttagcaccga 2040
      61 aagcggaggc caagacagta gagcaagagg ttgccgaaag ttcagtttct gaaggggagc 2100
      62 tgccaagcca tatggataca aaacatatag agcgaatacc gatggcatca gagcaggctc 2160
      63 agaccgtaag ccaacactta cacgcaggaa acctctctga actgggtaat ttaaacaata 2220
      64 tgaaccgaga cttagctttc catttgttga gagaagtctc tgattatttt cgccagagcg 2280
      65 aaccgcatag cccaatttca tttttgttag aaaaagcgat tcgatgggga tatttatcct 2340
      66 tacctgagtt gctgcgagaa atgatgtcgg aacaaaacgg tgacgctctt agtacgattt 2400
      67 ttaatgccgc cggattgaat catctcgatc aggttttgct gccggaggtg agtactccaa 2460
      68 cggtgggcat tgaaagcccc caaacacctc aagcgaagcc ttccgtttcg gatccgcgaa 2520
      69 gtgttgaaga gcatgtatct cagacttccc ctgtagatac ccaatctaag caagatcaaa 2580
E--> 70 aaccacaatc atccgctats drbcgtcggc tctgagttgg taattgtgtt taaaaaataa 2640
      71 ggaaaaatca tggcaagtat ttacatgcgt gtaagcggtc ttcaagttga gggcgcagcg 2700
      72 actatcggtc agctagaaac ggctgaaggt aaaaatgacg gttggtttgc aatcaactct 2760
      73 tactcttggg gtggcgctcg taacgttgct atggacatcg gtaacggcac caatgcggat 2820
      74 tcaggcatgg ttggcgtaag cgaagttagc gtaactaaag aagtcgatgg tgcttctgaa 2880
      75 gacctactgt cttatttatt caacccaggt aaagacggta aaactgttga ggttgcattt 2940
      76 actaagcctt ctaacgatgg tcaaggtgca gacgtttact tccaagttaa gctagaaaaa 3000
      77 gcacgtttag tttcttacaa cgtgagcggg actgacggat ctcaaccgta cgagagccta 3060
      78 tctctttctt acacttctat ttctcagaag catcactatg agaaagaagg tggtgaacta 3120
E--> 79 caaagcggtg gtgttgtgac ttacgaccta ccgaccggga aaatgactt ctggtaagta 3180
      80 attctttcat tagacatgcc acgttaattg gcatgtctat ttcatgaata tctcsdrcat 3240
      81 tttaggacac cgttatggca ttgaactcac aacataagcg cgttagtaag aaccgtgtca 3300
      82 gcatcaccta tgacgttgaa acgaatggcg ccgtaaagac gaaagagctg ccgtttgttg 3360
      83 ttggcgtcat tggcgacttt tcaggacaca aaccagaatc agaaaaagtt gatttagaag 3420
      84 agcgagagtt cacgggtatc gataaagaca acttcgatac agtgatgggg caaattcacc 3480
      85 cgcgtctttc gtacaaggtt gataacaagc ttgctaatga tgatagccag tttgaagtga 3540
W--> 86 acttgagcct ccgttcgatg aaagatttcc acccagagaa cttagttgat naaattgagc 3600
      87 cgcttaaag                                                       3609
```

Handwritten annotations (right margin): Stop codons are not acceptable in an amino acid sequence.

Handwritten (boxed): The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. specifically Sequence 4.

Handwritten (bottom right):
Sequence 1 Errors: n's must be enumerated in fields 221, 222 and 223.

1. Field 221 must be "unsure"
2. Field 222 must be a location in the sequence
3. Field 223 must be n = some string of possible unknowns

VERIFICATION SUMMARY   DATE: 10/17/2001
PATENT APPLICATION: US/09/915,706   TIME: 15:54:54

Input Set : **A:\5112.app**
Output Set: **N:\CRF3\10172001\I915706.raw**

```
L:11  M:270 C: Current Application Number differs, Replaced Application Number
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70  M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:79  M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:86  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:86  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:86  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
```

```
<400> 4
Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
 1               5                  10                 15

Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
            20                 25                 30

Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
            35                 40                 45

Ser Glu Lys Val Asp Leu Glu Glu Arg Glu Phe Thr Gly Ile Asp Lys
        50                 55                 60

Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
65                 70                 75                 80

Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn
                85                 90                 95

Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
            100                105                110

Xaa Ile Glu Pro Leu
            115
```